

|  |   |                                 |       |                          |
|--|---|---------------------------------|-------|--------------------------|
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| Run on:  | March 1, 2001, 16:26:02 ; Search time 29.37 Seconds | (without alignments)            |       |                          |
| Perfect score:   | US-09-331-631A-32                                   | 30.788 Million cell updates/sec |       |                          |
| Sequence:  | 1 CXXCXXXCXXXXXXCXXXCXXXC 28                        |                                 |       |                          |
| Scoring table:   | BLOSUM62DX  |                                 |       |                          |
| Searched:  | Gapop 10.0 , Gapext 0.5                             |                                 |       |                          |
| Total number of hits satisfying chosen parameters:   | 88757   |                                 |       |                          |
| Minimum DB seq length: 0   |   |                                 |       |                          |
| Maximum DB seq length: 200000000   |   |                                 |       |                          |
| Post-processing: Minimum Match 0%  |   |                                 |       |                          |
| Maximum Match 100%   |   |                                 |       |                          |
| Listing first 45 summaries   |   |                                 |       |                          |
| Swissprot_39: *  |   |                                 |       |                          |
| Pred. No. 1 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. |   |                                 |       |                          |
| SUMMARIES  |   |                                 |       |                          |
| Result No.   | Score   | Query Length                    | DB ID | Description              |
| 1  | 76  | 100.0                           | 74    | M84B_DRDOME              |
| 2  | 67  | 88.2                            | 55    | Q01643; drosophila       |
| 3  | 67  | 88.2                            | 55    | Q01644; drosophila       |
| 4  | 67  | 88.2                            | 57    | P56682; apis mellif      |
| 5  | 67  | 88.2                            | 58    | MT1_HOMMAM               |
| 6  | 67  | 88.2                            | 58    | MTL_SCYSE                |
| 7  | 67  | 88.2                            | 58    | MT2_CALSI                |
| 8  | 67  | 88.2                            | 58    | MTL_ASPEL                |
| 9  | 67  | 88.2                            | 58    | MTL_CARMA                |
| 10   | 67  | 88.2                            | 58    | P29499; homaruss ame     |
| 11   | 67  | 88.2                            | 59    | P02805; scylla serr      |
| 12   | 67  | 88.2                            | 63    | P55950; callinectes      |
| 13   | 67  | 88.2                            | 68    | P55951; astacus flu      |
| 14   | 67  | 88.2                            | 115   | P55948; carcinus ma      |
| 15   | 67  | 88.2                            | 157   | P55952; potamona pot     |
| 16   | 67  | 88.2                            | 178   | P55949; callinectes      |
| 17   | 67  | 88.2                            | 194   | Q01642; drosophila       |
| 18   | 67  | 88.2                            | 247   | Q01645; drosophila       |
| 19   | 67  | 88.2                            | 399   | Q46302; drosophila       |
| 20   | 67  | 88.2                            | 728   | P24834; Rhesus papi      |
| 21   | 67  | 88.2                            | 1133  | P20730; bombyx mori      |
| 22   | 67  | 88.2                            | 1255  | Q75590; homo sapien      |
| 23   | 67  | 88.2                            | 1257  | Q61999; mus musculu      |
| 24   | 67  | 88.2                            | 1363  | Q60751; mus musculu      |
| 25   | 67  | 88.2                            | 1367  | Q39017; arabisidispos    |
| 26   | 67  | 88.2                            | 1372  | P36607; schizosacch      |
| 27   | 67  | 88.2                            | 1372  | P04626; homo sapien      |
| 28   | 67  | 88.2                            | 1382  | P06499; ratus norvegicus |
| 29   | 67  | 88.2                            | 1383  | P02466; brachiofesto     |
| 30   | 67  | 88.2                            | 2813  | P08069; homo sapien      |
| 31   | 67  | 88.2                            | 2813  | P21062; ratus norvegicus |
| 32   | 66  | 88.2                            | 1     | P15208; mus musculu      |
| 33   | 66  | 88.2                            | 1     | P05213; homo sapien      |
|  |   |                                 |       | P1512; ratus norvegicus  |
|  |   |                                 |       | Q28395; canis familiaris |
|  |   |                                 |       | P04275; homo sapien      |
|  |   |                                 |       | P0251; mytilus edulis    |
|  |   |                                 |       | P80252; mytilus edulis   |
| RESULT   | 2   |                                 |       |                          |
| Db   | 12  |                                 |       | M84C_DRDOME              |
| ID   | N84C_DRDOME   |                                 |       | STANDARD;                |
| AC   | Q01641; Q9TA0;                                      |                                 |       | PRT;                     |
|  |   |                                 |       | 55 AA.                   |

|  |   |
|--|---|
| DT   | 01-JUL-1993 (Rel. 26, Last sequence update)   |
| DR   | 01-OCT-2000 (Rel. 40, Last annotation update)   |
| DE   | MALE-SPECIFIC SPERM PROTEIN MST84DC.  |
| GN   | MST84DC.  |
| OC   | Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriidae; Drosophilidae; Drosophila.   |
| RN   | [1]   |
| RP   | SEQUENCE FROM N.A.  |
| RC   | STRAIN=OREGON-R;  |
| RX   | MEDLINE=92102953; PubMed=1684716;   |
| RT   | "A cluster of four genes selectively expressed in the male germ line of <i>Drosophila melanogaster</i> ";   |
| RL   | Mech. Dev. 35:143-151(1991);  |
| RN   | [2]   |
| RP   | SEQUENCE FROM N.A.  |
| RC   | STRAIN=BERKELEY;  |
| RX   | MEDLINE=20196006; PubMed=10731132;  |
| RA   | Adams M.D., Celikin S.E., Holt R.A., Evans C.A., Gocayne J.D., Almanantes P.G., Schaefer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazquez R.G., Chapple M., Pfeiffer B.D., Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abrial J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D., Ballivet R.M., Barlow A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Beres P.V., Berman B.P., Bhandari D., Bolshakov S., Borukova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burt K.C., Busam H., Cadieu E., Center A., Chandra I., Cherry J.M., Cowley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Durbin R.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W., Foster C., Gabrilian A.E., Garg N.S., Gelbart W.M., Glusser R.K., Globek A., Goss F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitt A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Mishina N.V., Mobarry C., Morris J., Mosbrefi A., Nelson S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.A., Nixon K., Nusskern D.R., Pacieb J.M., Palazzoio M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Ramington K., Saunders R.D.C., Schaefer P., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svartkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; |
| RT   | "The genome sequence of <i>Drosophila melanogaster</i> ";   |
| RL   | Science 287:2183-2193 (2000);   |
| CC   | -!- TISSUE SPECIFICITY: TESTIS  |
| CC   | -!- DEVELOPMENTAL STAGE: PRIMARY SPERMATOCYTES  |
| CC   | -!- DOMAIN: THIS PROTEIN IS MOSTLY COMPOSED OF REPETITIVE C-G-P MOTIFS.   |
| CC   | -!- SIMILARITY: BELONGS TO THE MST(3)CGP FAMILY.  |
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| RESULT   | 4   |
| MT2_SCYSE  | STANDARD; PRT; 57 AA.   |
| ID   | MT2_SCYSE   |
| AC   | P072806;  |
| DT   | 21-JUL-1986 (Rel. 01, Created)  |
| DT   | 21-JUL-1986 (Rel. 01, Last sequence update)   |
| DT   | 01-NOV-1997 (Rel. 35, Last annotation update)   |
| DE   | METALLOTHIONEIN-II (MT-II).   |
| OS   | Scyllia serrata (Mud crab).   |
| OC   | Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura; Brachyrachidea; Portunidae; Portunidae; Scyllia.   |
| SQ   | SEQUENCE 55 AA; 52.25 MW; 95A12F3ACE88BD6C CRC64;   |
| QY   | 1 CXXXXXXXCCCCCCCCCCCCXXXXXX 27<br> :::    :::    :::    :::    :::<br>3 CGCGGCCGYYCCGPGCPGPGPC 29  |
| Db   | Query Match 88 2%; Score 67; DB 1; Length 55;<br>Best Local Similarity 18 5%; Pred. No. 22; Mismatches 0; Indels 0; Gaps 0;<br>Matches 5; Conservative 22; Mismatches 0; Indels 0; Gaps 0;  |
| QY   | 1 XXCCCCXXXXXXXXXXXXXXX 27<br> :::    :::    :::    :::<br>3 CGCGGCCGYYCCGPGCPGPGPC 29  |
| Db   | Query Match 88 2%; Score 67; DB 1; Length 55;<br>Best Local Similarity 18 5%; Pred. No. 22; Mismatches 0; Indels 0; Gaps 0;<br>Matches 5; Conservative 22; Mismatches 0; Indels 0; Gaps 0;  |
| QY   | 1 XXCCCCXXXXXXXXXXXXXXX 28<br> :::    :::    :::    :::<br>3 CGCGGCCGYYCCGPGCPGPGPC 36  |
| Db   | Query Match 88 2%; Score 67; DB 1; Length 55;<br>Best Local Similarity 18 5%; Pred. No. 22; Mismatches 0; Indels 0; Gaps 0;<br>Matches 5; Conservative 22; Mismatches 0; Indels 0; Gaps 0;  |
| QY   | 1 XXCCCCXXXXXXXXXXXXXXX 28<br> :::    :::    :::    :::<br>3 CGCGGCCGYYCCGPGCPGPGPC 36  |
| Db   | Query Match 88 2%; Score 67; DB 1; Length 55;<br>Best Local Similarity 18 5%; Pred. No. 22; Mismatches 0; Indels 0; Gaps 0;<br>Matches 5; Conservative 22; Mismatches 0; Indels 0; Gaps 0;  |
| CC   | AMCI_APME 3   |
| ID   | AMCI_APME   |
| AC   | P5682;  |
| DT   | 15-JUL-1999 (Rel. 38, Created)  |
| DT   | 30-MAY-2000 (Rel. 39, Last annotation update)   |
| DE   | CHMORRPSIN INHIBITOR (AMCI).  |
| OS   | Apis mellifera (Honeybee).  |
| OC   | Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apidae; Apidae; Apis.  |
| RN   | [1]   |
| RP   | SEQUENCE AND STRUCTURE BY NMR.  |
| RC   | TISSUE=HEMOLYMPH;   |
| RX   | MEDLINE=99339935; PubMed=10411628;  |
| RA   | Bania J., Stachowak D., Polanowski A.;  |
| RT   | "Primary structure and properties of the cathepsin G/chymotrypsin inhibitor from the larval hemolymph of <i>Apis mellifera</i> ".;  |
| RL   | Eur. J. Biochem. 262:680-687 (1999).  |
| CC   | -!- FUNCTION: CHYMOTRYPSIN/CATHEPSIN G INHIBITOR.   |
| CC   | -!- SUBCELLULAR LOCATION: SECRETED.   |
| DR   | PDB: 1CCV; 1Z-MR-99. -.   |
| DR   | INTERPRO: IPRO02919; -.   |
| DR   | PFAM: PF01826; TIL_1.   |
| KW   | Serine protease inhibitor; 3D-structure.  |
| FT   | DISULFID 3 36   |
| FT   | DISULFID 12 32  |
| FT   | DISULFID 16 28  |
| FT   | DISULFID 20 56  |
| FT   | DISULFID 38 50  |
| SQ   | SEQUENCE 56 AA; 5973 MW; 092B2815AE6B2B7F CRC64;  |
| Query Match 88 2%; Score 67; DB 1; Length 55;<br>Best Local Similarity 18 5%; Pred. No. 23; Mismatches 0; Indels 0; Gaps 0;<br>Matches 5; Conservative 22; Mismatches 0; Indels 0; Gaps 0; |   |
| QY   | 2 XXCCCCXXXXXXXXXXXXXXX 28<br> :::    :::    :::    :::<br>3 CGCGGCCGYYCCGPGCPGPGPC 36  |
| Db   | Query Match 88 2%; Score 67; DB 1; Length 55;<br>Best Local Similarity 18 5%; Pred. No. 22; Mismatches 0; Indels 0; Gaps 0;<br>Matches 5; Conservative 22; Mismatches 0; Indels 0; Gaps 0;  |

RN [1]  
 RP SQUENCE.  
 RX MEDLINE=94318629; PubMed=8043573;  
 RA Zhu S., Derose E.F., Mulien G.P., Petering D.H., Shaw C.F. III;  
 RT "sequential proton resonance assignments and metal cluster topology  
 RA Lerch K., Ammer D., Olafson R.W.;  
 RT "Crab metallothionein. Primary structures of metallothioneins 1 and  
 RT 2.";  
 RL J. Biol. Chem. 257:2420-2426(1982).  
 CC -!- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE  
 RESIDUES THAT BIND VARIOUS HEAVY METALS. CLASS I MTS IN MARINE  
 CRUSTACEA ARE INVOLVED IN THE SEQUESTRATION OF ELEVATED  
 LEVELS OF HEAVY-METAL IONS. BINDS 6 METAL IONS. KNOWN  
 CC -!- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.  
 CC PIR: A03284; SMKDS.  
 DR HSSP: P55949; 1DMF.  
 DR INTERPRO: IPR002045; -.  
 DR PEAM: PF00131; metalthio; 1.  
 DR PRINTS: PR00858; MTCRUSTACEAN.  
 DR KW Metal-binding; Metal-thiolate cluster; Chelation.  
 FT DOMAIN 1 Metal 28  
 FT DOMAIN 29 57 ALPHA.  
 FT METAL 4 4 CLUSTER B.  
 FT METAL 5 5 CLUSTER B.  
 FT METAL 9 9 CLUSTER B.  
 FT METAL 11 11 CLUSTER B.  
 FT METAL 15 16 CLUSTER B.  
 FT METAL 20 20 CLUSTER B.  
 FT METAL 22 22 CLUSTER B.  
 FT METAL 25 25 CLUSTER B.  
 FT METAL 27 27 CLUSTER B.  
 FT METAL 30 30 CLUSTER A.  
 FT METAL 33 33 CLUSTER A.  
 FT METAL 37 37 CLUSTER A.  
 FT METAL 39 39 CLUSTER A.  
 FT METAL 45 45 CLUSTER A.  
 FT METAL 49 49 CLUSTER A.  
 FT METAL 53 53 CLUSTER A.  
 FT METAL 55 55 CLUSTER A.  
 FT METAL 56 56 CLUSTER A.  
 SQ SEQUENCE 57 AA; 6109 MW; 8C2B3F6A6BAA3611 CRC64;

RESULT 5  
 Query Match 88.2%; Score 67; DB 1; Length 57;  
 Best Local Similarity 18.5%; Pred. No. 23;  
 Matches 5; Conservative 22; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CXCCXXXCXXXXXXCXXXXXXX 27  
 Db 30 CBQCSSGCKCANKEDCRKTCSKPCSCC 56

RN [1]  
 ID MTL\_HOMAM STANDARD; PRT; 58 AA.  
 AC P29499;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DE METALLOTHIONINE-1 (CMT-1).  
 OS Homarus americanus (American lobster).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;  
 OC Nephropoidea; Nephropidae; Homarus.  
 RN [1]  
 RP SQUENCE.  
 RC TISSUE=HEPATOPANCREAS;  
 RX MEDLINE=89215793; PubMed=2709004;  
 RA Brouwer M., Winge D.R., Gray W.R.;  
 RT "Structural and functional diversity of copper-metallothioneins from  
 RT the American Lobster Homarus americanus.";  
 RL J. Inorg. Biochem. 35:289-303(1989).  
 RN [2]  
 RP STRUCTURE BY NMR.

RN [1]  
 RP SQUENCE.  
 RX MEDLINE=94318629; PubMed=8043573;  
 RA Zhu S., Derose E.F., Mulien G.P., Petering D.H., Shaw C.F. III;  
 RT "sequential proton resonance assignments and metal cluster topology  
 of lobster metallothionein-1.";  
 RL Biochemistry 33:8858-8865(1994).  
 CC -!- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE  
 RESIDUES THAT BIND VARIOUS HEAVY METALS. THE DIFFERENT FORMS OF  
 LOBSTER METALLOTHIONEINS MAY HAVE DIFFERENT BIOLOGICAL FUNCTIONS.  
 CLASS I MTS IN MARINE CRUSTACEA ARE INVOLVED IN THE SEQUESTRATION  
 OF ELEVATED LEVELS OF HEAVY-METAL IONS. BINDS 6 METAL IONS. KNOWN  
 CC -!- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.  
 CC PIR: A37039; A37039.  
 DR HSSP: P55949; 1DMF.  
 DR INTERPRO: IPR003019; -.  
 DR PEAM; PF00131; metalthio; 1.  
 DR PRINTS: PR00858; MTCRUSTACEAN.  
 DR KW Metal-binding; Metal-thiolate cluster; Chelation; copper; Cadmium.  
 FT DOMAIN 1 Metal 28 ALPHA.  
 FT DOMAIN 29 58 ALPHA.  
 FT METAL 4 4 CLUSTER B.  
 FT METAL 5 5 CLUSTER B.  
 FT METAL 9 9 CLUSTER B.  
 FT METAL 11 11 CLUSTER B.  
 FT METAL 16 16 CLUSTER B.  
 FT METAL 20 20 CLUSTER B.  
 FT METAL 22 22 CLUSTER B.  
 FT METAL 25 25 CLUSTER B.  
 FT METAL 27 27 CLUSTER B.  
 FT METAL 30 30 CLUSTER A.  
 FT METAL 33 33 CLUSTER A.  
 FT METAL 37 37 CLUSTER A.  
 FT METAL 39 39 CLUSTER A.  
 FT METAL 45 45 CLUSTER A.  
 FT METAL 49 49 CLUSTER A.  
 FT METAL 53 53 CLUSTER A.  
 FT METAL 55 55 CLUSTER A.  
 FT METAL 56 56 CLUSTER A.  
 SQ SEQUENCE 58 AA; 5975 MW; 176ABA60A32F96 CRC64;

RESULT 6  
 Query Match 88.2%; Score 67; DB 1; Length 58;  
 Best Local Similarity 18.5%; Pred. No. 23;  
 Matches 5; Conservative 22; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CXCCXXXCXXXXXXCXXXXXXX 27  
 Db 30 CEKCTSCKCPSKDECAKTCSPCSCC 56

RN [1]  
 ID MTL\_SCYSE STANDARD; PRT; 58 AA.  
 AC P02805;  
 DT 21-JUL-1996 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE METALLOTHIONINE-1 (Mr-I).  
 OS Scylla serrata (Mud crab).  
 OC Eukaryota; Metazoa; Arthropoda; Crustaceans; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 OC Brachyura; Portunoidea; Portunidae; Scylla.  
 RN [1]  
 RP SQUENCE.  
 RX MEDLINE=892142340; PubMed=7061431;  
 RA Lerch K., Ammer D., Olafson R.W.;  
 RT "Crab metallothionein. Primary structures of metallothioneins 1 and  
 RT 2.";  
 RL J. Biol. Chem. 257:2420-2426(1982).  
 CC -!- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE  
 RESIDUES THAT BIND VARIOUS HEAVY METALS. CLASS I MTS IN MARINE  
 CC CRUSTACEA ARE INVOLVED IN THE SEQUESTRATION OF ELEVATED LEVELS









Search completed: March 1, 2001, 16:26:02  
 Job time: 399 sec

RL Science 297:2185-2195 (2000).  
 CC -!- FUNCTION: RESPONSIBLE FOR PHYSIOLOGICAL AND BEHAVIORAL CHANGES IN  
 CC MATED FEMALE FLEES.  
 CC -!- SUBCELLULAR LOCATION: SECRETED (POTENTIAL).

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 DR EMBL; U85163; AAB96387.1; -.  
 DR EMBL; AE013475; AAF7683.1; -.  
 DR FLYBASE; FBgn0020509; ACp62F.  
 KW Behavior.

SQ SEQUENCE: 115 AA; 12570 MW; 4326AA6FFC32291D CHC64;

| Query | Match                 | Score  | DB         | Length |
|-------|-----------------------|--------|------------|--------|
|       | Best Local Similarity | 88.2%  | 1;         | 115;   |
|       | Matches               | 18.5%; | Pred. No.  | 37;    |
|       |                       | 5;     | Indels     | 0;     |
|       |                       |        | Mismatches | 0;     |
|       |                       |        | Gaps       | 0;     |

Qy 2 XXCXAXCXXXXXXCXXXCXXX 28  
 Qy :::::1:::1:::1:::1:::1:::1  
 Db 41 TECPACPETCEYSGNGPCVVKMGAFC 67

RESULT 15

VES\_RHPV1  
 VES\_RHPV1 STANDARD; PRT; 157 AA.

ID P24834;  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE PROBABLE E5 PROTEIN.

GN E5.  
 OS Rhesus Papillomavirus type 1 (Rhpv 1).  
 OC Papovaviridae; Papillomavirus.  
 RN [1]  
 RP SEQUENCE FROM N.A.

RX MEDLINE=91135018; PubMed=1847767;  
 RA Ostrow R.S., Labresen K.V., Faras A.J.;  
 RT "Characterization of the complete RHPV 1 genomic sequence and an  
 RT integration locus from a metastatic tumor.";  
 RL Virology 181:424-429(1991).

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 DR EMBL; M60184; AAA79315.1; ALT-SEQ.  
 DR EMBL; M60184; AAA79316.1; ALT-SEQ.  
 DR PIR; F3803; W5WLR1.  
 KW Early Protein.

SQ SEQUENCE: 157 AA; 17398 MW; ACT7AA67158844686 CRC64;

| Query | Match                 | Score            | DB         | Length |
|-------|-----------------------|------------------|------------|--------|
|       | Best Local Similarity | 88.2%; Score     | 67;        | 157;   |
|       | Matches               | 18.5%; Pred. No. | 46;        |        |
|       |                       | 5;               | Mismatches | 0;     |
|       |                       |                  | Indels     | 0;     |
|       |                       |                  | Gaps       | 0;     |